

AMENDMENTS TO THE CLAIMS:

Please replace the claims with the claims provided in the listing below wherein status, amendments, additions and cancellations are indicated.

1. (Currently amended) ~~Tools~~ Method for the ~~diagnostics, diagnosis~~ and/or molecular definition ~~[[and]]~~ and/or therapy development for chronic inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in the ~~human~~ humans or animals, ~~whereat these tools are realized under~~ the method comprising, for humans, employment of the substances which are sequences of single genes, a selection of genes or the entirety of the genes ~~mentioned in table~~ of Table 1 and and/or of the genes coding for the proteins ~~mentioned in table~~ of Table 2 and/or employment of partial or complete sequences of single, a selection, or the entirety of proteins and peptides deduced from said gene sequences, and, for animals, employment of substances which are homologs of said substances for humans.

2. (Currently amended) ~~Tools~~ Method according to claim 1, ~~characterized in that they include~~ in which the gene sequences, ~~which in respect~~ to their sequence are identical with the ~~genes mentioned in table 1 or with the~~ genes coding for the proteins mentioned in table 2, or ~~which~~ have a respective

sequence identity of at least 80% in the protein-coding regions of, the genes of Table 1 or the genes coding for the proteins of Table 2.

3. (Currently amended) ~~Tools~~ Method according to ~~claims 1 and claim 2, characterized in that they include~~ wherein the substances comprise sequence sections or partial sequences, which in respect to their sequence are identical with ~~the genes mentioned in table 1 and the genes subsumed under claim 2, or~~ which have a sequence identity of at least 80% with the respective sections of, the mentioned genes of Table 1 and the genes of claim 2.

4. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 3, ~~characterized in that, they are based on the employment of a~~ further comprising

[[4.1.]] a High-Throughput method of (micro-) array-hybridisation or

[[4.2.]] a High-Throughput method using techniques of ~~[[the]]~~ polymerase chain reaction for (semi-) quantification.

5. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 3, ~~characterized in that they are based on the employment of~~ further comprising using a labeled patient sample and a second, differently labeled

control sample[,] ~~which is used~~ for a comparative double hybridisation to a ~~(micro-)~~ an array together with the patient sample to effect a ~~[[()]]~~ comparative red/green hybridisation~~[[()]]~~.

6. (Currently amended) ~~Tools~~ Method according to ~~claims 1 to 5~~ for ~~diagnostic purposes, characterized in that they are based on the employment~~ claim 1, wherein said method is for diagnosis and the substances comprise partial or complete sequences of single, a selection, or the entirety of proteins or peptides deduced from the said gene sequences ~~in claims 1 to 3~~.

7. (Currently amended) ~~Tools~~ Method according to claim 6, ~~characterized in that they are based on the employment of~~ wherein the substances comprise single proteins, a selection of proteins or the entirety of the proteins ~~mentioned in table~~ of Table 2.

8. (Currently amended) ~~Tools~~ Method according to ~~claims~~ claim 6 and or 7, characterized in that they are based on wherein the use of partial protein or peptide sequences of single proteins, a selection of proteins or the entirety of the ~~proteins mentioned in table~~ comprise partial sequences of proteins deduced from the genes of Table 1.

9. (Currently amended) ~~Tools~~ Method according to ~~claims claim~~ 6 to 8 or 7, characterized in that they include proteins or partial protein sequences, ~~which~~ wherein the substances in respect to their sequence are identical with or have a sequence identity of at least 80% with the proteins deduced ~~in table from~~ the genes of Table 1 or with the proteins ~~mentioned in table of Table 2~~ [[.]] or ~~which have a respective sequence identity of at least 80%.~~

10. (Currently amended) ~~Tools~~ Method according to ~~claims claim~~ 6 to 9 or 7, characterized in that they are based on the employment of further comprising [[10.1.]] High-Throughput methods ~~in the analyties~~ for analysis of protein expression [[()] comprising high definition, two-dimensional protein gel electrophoresis, MALDI techniques~~[[()]]~~ or [[10.2]] High-Throughput methods ~~in the~~ for protein spotting ~~technique~~ [[()] by means of protein arrays~~[[()]]~~ designed to screen for screening for auto-antibodies ~~as diagnostic tools~~ for diagnosis of inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in ~~the human~~ humans or [[10.3]] High-Throughput methods ~~in the technique of~~ for protein spotting [[()] by means of protein arrays~~[[()]]~~ designed to screen for screening for autoreactive T cells ~~as diagnostic tools~~ for diagnosis of inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in ~~the human~~ humans or

[[10.4]] Non-High-Throughput methods ~~in the technique of~~ for protein spotting ~~designed to screen~~ for screening for autoreactive T cells ~~as diagnostic tools~~ for diagnosis of inflammatory joint diseases and other inflammatory, infectious or tumorous diseases ~~in the human~~ humans.

11. (Currently amended) ~~Tools~~ Method according to ~~claims~~ claim 6 to ~~9 or 7,~~ characterized ~~in that they are based on the~~ further comprising employment of antibodies[[,]] which are specific for ~~proteins or~~ said partial or complete sequences ~~specified in claims 6 to 9 of single, a selection or entirety of~~ said proteins or peptides deduced from said gene sequences.

12. (Currently amended) ~~Tools according to claims~~ Method according to claim 1 to ~~11,~~ characterized ~~in that they are based on the use of the~~ corresponding homologous sequences of another species for the analytics in animal experiments or for the diagnostics in animals with inflammatory joint diseases and other inflammatory, infectious or tumorous diseases for animals, wherein said substances are said homologs of said substances for humans.

13. (Currently amended) ~~Tools according to claims~~ Method according to claim 6 to ~~11 as diagnostic tools for the detection of genetic alterations~~ [[()]]or

7, wherein mutations in the said genes mentioned in claims 1 to 3 or alterations in the regulatory sequences (promoter, enhancer, silencer, specific sequences for binding further regulatory factors) of these said genes are detected.

14. (Currently amended) ~~Tools~~ Method according to ~~claims~~ claim 6 to 11 and 13 for the detection of genetic alterations or 7, wherein mutations in the said genes coding for the proteins mentioned in table of Table 2 or alterations in the regulatory sequences (promoter, enhancer, silencer, specific sequences for binding further regulatory factors) of these said genes are detected.

15. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 ~~for the 3, 6 and 7, wherein~~ molecular ~~definition~~ definitions of inflammatory joint diseases and other inflammatory, infectious or tumorous said diseases in the human, ~~whereat these tools are realized under the employment of the genes or DNA-sequences mentioned in the claims 1-3 or the respective, deduced proteins or peptides and of the proteins and partial protein sequences from claims 6 to 9 or their corresponding, coding gene sequences~~ humans are determined.

16. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 ~~for the selection of a therapy 3, wherein therapies for said for~~ inflammatory joint diseases and other inflammatory, infectious or tumorous diseases in the human, whereat these tools employ the genes or DNA-sequences mentioned in claims 1-3 or the respective, deduced proteins or peptides are selected.

17. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to ~~[[5]]~~ 3, wherein progress of therapies for monitoring the progression/controlling the therapy of inflammatory joint said diseases and other inflammatory, infectious or tumorous diseases in the human, whereat these tools employ the genes or DNA-sequences mentioned in claims 1-3 or the respective, deduced proteins or peptides is monitored and the therapies are controlled based on said monitoring.

18. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 ~~as molecular tools for the development of 3, wherein~~ therapy concepts are developed, which include the said therapy concepts comprising direct or indirect impact on the expression of the said genes or gene sequences ~~mentioned in claims 1-3~~.

19. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 and 18 ~~for the development of 3, wherein~~ therapy concepts are developed, ~~which include the~~ said therapy concepts comprising direct or indirect impact on the expression of the said proteins or partial protein sequences ~~mentioned in~~ claims 6 to 9.

20. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 and 18 to 19 ~~for the development of 3, wherein~~ therapy concepts are developed, ~~which include the~~ said therapy concepts comprising direct or indirect impact on the autoreactive T cells being directed against the said proteins or partial protein sequences ~~mentioned in~~ claims 8-11.

21. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 and 18 to 20 ~~for affecting the 3, wherein~~ biological action of the proteins deduced from the said gene sequences ~~mentioned in~~ claims 1 to 3 is affected.

22. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 and 18 to 21 ~~for affecting the 3, wherein~~ direct molecular regulatory circuits/pathways, in which the said genes ~~mentioned in~~ claims 1-3 and the

respective[[,]] ~~deduced~~ proteins deduced therefrom[[,]] are involved, are affected.

23. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 and 18 to 22 for ~~developing therapy concepts under the design and employment of 3, further comprising constructing and applying~~ interpretation algorithms ~~using the mentioned genes and sequences and their regulatory mechanisms, in order to recognize or predict therapy concepts, therapy effects, therapy optimizations or diseases prognoses.~~

24. (Currently amended) ~~Tools~~ Method according to any one of claims 1 to 5 and 18 to 22 for 3, further comprising developing biologically active drugs for said diseases (Biologicals) ~~under the employment of genes, gene sequences, the regulation of genes or gene sequences, or under the employment of proteins, protein sequences, fusion proteins according to claims 1 to 3 and 6 to 9 or under the employment of antibodies or autoreactive T cells according to claims 10 to 14.~~

25. (Currently amended) ~~Array as a molecular tools~~ A molecular tool ~~comprised of an array~~ A molecular tool comprised of an array, the array being

comprised of different antibodies or molecules with a comparable protein-specific binding behaviour, ~~which are intended for the detection of the~~ antibodies or molecules being capable of detecting the entirety of or a selection of the proteins deduced from the genes in ~~table~~ Table 1 or ~~for the detection of~~ the entirety of or a selection of ~~[[the]]~~ said proteins ~~in table~~ of Table 2.

26. (Canceled)

27. (New) Method according to any one of claims 1 to 3, wherein said substances are employed in connection with analysis of blood samples or tissue samples in medical diagnosis.

28. (New) Method according to any one of claims 1 to 3, wherein said substances are employed in connection with analysis of tissue samples in diagnosing and/or assessing the activity and/or developing a prognosis for and/or developing therapeutic options for said diseases.

29. (New) Method according to any one of claims 1 to 3, wherein said substances are employed in connection with selection of therapies for said diseases.